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OCT 03 2003

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/667,859A

DATE: 09/30/2003

TIME: 07:50:47

Input Set : A:\08341.ST25.txt

Output Set: N:\CRF4\09302003\I667859A.raw

3 <110> APPLICANT: Kubin, Marek Z.  
 4 Goodwin, Raymond G.  
 6 <120> TITLE OF INVENTION: NK Cell Activation Inducing Ligand (NAIL) DNA and  
 Polypeptides,

7 and Uses Thereof

9 &lt;130&gt; FILE REFERENCE: AMGEN-08341

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/667,859A

12 &lt;141&gt; CURRENT FILING DATE: 2000-09-20

14 &lt;160&gt; NUMBER OF SEQ ID NOS: 13

16 &lt;170&gt; SOFTWARE: PatentIn version 3.2

18 &lt;210&gt; SEQ ID NO: 1

19 &lt;211&gt; LENGTH: 1095

20 &lt;212&gt; TYPE: DNA

21 &lt;213&gt; ORGANISM: Homo sapiens

23 &lt;400&gt; SEQUENCE: 1

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26	ggatgccagg	gatcagctga	ccatgtggtt	agcatctcgg	gagtgcctct	tcagttacaa	120
28	ccaaacagca	tacagacgaa	ggttgacagc	attgcatgga	agaagttgct	gccctcacia	180
30	aatggatttc	atcacatatt	gaagtgggag	aatggctctt	tgccttccaa	tacttccaat	240
32	gatagattca	gttttatagt	caagaacttg	agtcttctca	tcaaggcagc	tcagcagcag	300
34	gacagtggcc	tctactgcct	ggaggtcacc	agtatatctg	gaaaagtcca	gacagccacg	360
36	ttccagggtt	ttgtatttga	taaagttgag	aaaccccgcc	tacaggggca	ggggaagatc	420
38	ctggacagag	ggagatgcc	agtggctctg	tcttgcttgg	tctccaggga	tggcaatgtg	480
40	tcctatgctt	ggtacagagg	gagcaagctg	atccagacag	cagggaacct	cacctacctg	540
42	gacgaggagg	ttgacattaa	tggcactcac	acatactact	gcaatgtcag	caatcctggt	600
44	agctgggaaa	gccacaccct	gaatctcact	caggactgtc	agaatgcca	tcaggaattc	660
46	agattttggc	cgtttttggt	gatcatcggt	attctaagcg	cactgttcct	tggcaccctt	720
48	gcctgcttct	gtgtgtggag	gagaaagagg	aaggagaagc	agtcagagac	cagtccaag	780
50	gaatttttga	caattttacga	agatgtcaag	gatctgaaaa	ccaggagaaa	tcacgagcag	840
52	gagcagactt	ttcctggagg	ggggagcacc	atctactcta	tgatccagtc	ccagtcttct	900
54	gctcccacgt	cacaagaacc	tgcatataca	ttatattcat	taattcagcc	ttccaggaag	960
56	tctggatcca	ggaagaggaa	ccacagccct	tccttcaata	gcactatcta	tgaagtgatt	1020
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63 &lt;210&gt; SEQ ID NO: 2

64 &lt;211&gt; LENGTH: 365

65 &lt;212&gt; TYPE: PRT

66 &lt;213&gt; ORGANISM: Homo sapiens

68 &lt;400&gt; SEQUENCE: 2

70 Met Leu Gly Gln Val Val Thr Leu Ile Leu Leu Leu Leu Lys Val

71 1 5 10 15

74 Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile

75 20 25 30

78 Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val

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82 Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
83          50          55          60
86 His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
87 65          70          75          80
90 Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
91          85          90          95
94 Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
95          100          105          110
98 Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
99          115          120          125
102 Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly
103          130          135          140
106 Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val
107 145          150          155          160
110 Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn
111          165          170          175
114 Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr
115          180          185          190
118 Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn
119          195          200          205
122 Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro
123          210          215          220
126 Phe Leu Val Ile Ile Val Ile Leu Ser Ala Leu Phe Leu Gly Thr Leu
127 225          230          235          240
130 Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu
131          245          250          255
134 Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu
135          260          265          270
138 Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly
139          275          280          285
142 Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser
143          290          295          300
146 Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys
147 305          310          315          320
150 Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile
151          325          330          335
154 Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg
155          340          345          350
158 Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser
159          355          360          365
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 2440
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 3
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170 aggttgcaag gcagttctgc tccccatcgt cctcttgctg actggggact gctgagcccg 120
172 tgcacggcag agagtctggt ggggtggagg ggctggcctg gccctctgt cctgtggaaa 180

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174 tgctggggca agtgggcacc ctcatactcc tcctgctcct caagggtgtat cagggcaaa 240
176 gatgccaggg atcagctgac catgtggtta gcatctcggg agtgcctctt cagttacaac 300
178 caaacagcat acagacgaag gttgacagca ttgcatggaa gaagttgctg ccctcacaaa 360
180 atggatttca tcacatattg aagtgggaga atggctcttt gccttccaat acttccaatg 420
182 atagattcag ttttatagtc aagaacttga gtcttctcat caaggcagct cagcagcagg 480
184 acagtggcct ctactgcctg gaggtcacca gtatatctgg aaaagttcag acagccacgt 540
186 tccaggtttt tgtatttgat aaagttgaga aaccccgctt acaggggcag gggaagatcc 600
188 tggacagagg gagatgccaa gtggctctgt cttgcttggg ctccagggat ggcaatgtgt 660
190 cctatgcttg gtacagaggg agcaagctga tccagacagc agggaacctc acctacctgg 720
192 acgaggaggt tgacattaat ggcactcaca catatacctg caatgtcagc aatcctgtta 780
194 gctgggaaag ccacaccctg aatctcactc aggactgtca gaatgcccat caggaattca 840
196 gattttggcc gtttttggg atcatcgtga ttctaagcgc actgttcctt ggcacccttg 900
198 cctgcttctg tgtgtggagg agaaagagga aggagaagca gtcagagacc agtcccaagg 960
200 aatttttgac aattttacgaa gatgtcaagg atctgaaaac caggagaaat cacgagcagg 1020
202 agcagacttt tcctggaggg gggagcacca tctactctat gatccagtcc cagtcttctg 1080
204 ctcccacgtc acaagaacct gcatatacat tatattcatt aattcagcct tccaggaagt 1140
206 ctggatccag gaagaggaac cacagccctt ccttcaatag cactatctat gaagtgattg 1200
208 gaaagagtca acctaaagcc cagaaccctg ctcgattgag ccgcaaagag ctggagaact 1260
210 ttgatgttta ttctagttg ctgcagcaat tctcaccttt cttgcacatc agcatctgct 1320
212 ttgggaattg gcacagtga tgacggcaca ggagtctcta tagaactctt cctagtctgg 1380
214 agaggatatg gaaatttggt cttgttctat attttgtttt gaaaatgatg tctaacaacc 1440
216 atgataagag caaggctgtt aaataatatc ttccaattta cagatcagac atgaatgggt 1500
218 ggaggggtta ggttggtcac aaaaggccac attccaagta tttgtaatct agaaagtgtt 1560
220 atgtaagtga tgttattagc atcgagattc cctccacctg attttcaagc tgtcacttgt 1620
222 ttcttttctt cccctctctg ggttgactgc atttctagac tctcgccggc ccaggcccat 1680
224 ctccaaaagc aagaggaagg aatgataatg gtgactcagg ggaagaagaa acagccctcc 1740
226 tctgaaagcc tggactgtcc ggctgtgaac tggctggcag gttctgcacg tgggtggggg 1800
228 ccagggcctg ggctttactc aattgcagag aaaaaacttt ctccctgcat ctcatacctt 1860
230 tacctctggc cagttggcca ccagggggag tgggctgaag ggagagtaga tgggtgaaaag 1920
232 caagcccatc tctgagtaga aaaatcaccc agagcacatg ctgacctgat aactgggggtg 1980
234 ttgagaccag ctttgtccat ggtatgatgt ttgatttatg aagacgcatt gttagaaatc 2040
236 catttggctt cttcatagaa gtggcttccc agaggaagag gcctctcaga aaccatgttc 2100
238 tatttaagtt ctgagtcctg atgagtgttc cccaggatgc acattgaagg gagggctcag 2160
240 gcagctgagg gctgagaatg aggcagttgg aatctagaca ctatgctggg ttccctgagt 2220
242 cgtcaggcca gacatttcaa caaggctgtg gggagcaggg ctgtgactct ggctgagccc 2280
244 aggaaagcga caagggtgaa ctgggagagg acttactcag agacccaac aggtgatact 2340
246 gcacaaagcc tggttcttca attttcctac cctgtatcta acataggagt ttcatataaa 2400
248 acggtgatat catgcagatg cagtctgaat tccttgccgt 2440

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251 &lt;210&gt; SEQ ID NO: 4

252 &lt;211&gt; LENGTH: 398

253 &lt;212&gt; TYPE: PRT

254 &lt;213&gt; ORGANISM: Mus musculus

256 &lt;400&gt; SEQUENCE: 4

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258 Met Leu Gly Gln Ala Val Leu Phe Thr Thr Phe Leu Leu Leu Arg Ala
259 1 5 10 15
262 His Gln Gly Gln Asp Cys Pro Asp Ser Ser Glu Glu Val Val Gly Val
263 20 25 30
266 Ser Gly Lys Pro Val Gln Leu Arg Pro Ser Asn Ile Gln Thr Lys Asp
267 35 40 45

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270 Val Ser Val Gln Trp Lys Lys Thr Glu Gln Gly Ser His Arg Lys Ile
271      50                      55                      60
274 Glu Ile Leu Asn Trp Tyr Asn Asp Gly Pro Ser Trp Ser Asn Val Ser
275 65                      70                      75                      80
278 Phe Ser Asp Ile Tyr Gly Phe Asp Tyr Gly Asp Phe Ala Leu Ser Ile
279                      85                      90                      95
282 Lys Ser Ala Lys Leu Gln Asp Ser Gly His Tyr Leu Leu Glu Ile Thr
283                      100                     105                     110
286 Asn Thr Gly Gly Lys Val Cys Asn Lys Asn Phe Gln Leu Leu Ile Leu
287                      115                     120                     125
290 Asp His Val Glu Thr Pro Asn Leu Lys Ala Gln Trp Lys Pro Trp Thr
291                      130                     135                     140
294 Asn Gly Thr Cys Gln Leu Phe Leu Ser Cys Leu Val Thr Lys Asp Asp
295 145                      150                      155                      160
298 Asn Val Ser Tyr Ala Phe Trp Tyr Arg Gly Ser Thr Leu Ile Ser Asn
299                      165                      170                      175
302 Gln Arg Asn Ser Thr His Trp Glu Asn Gln Ile Asp Ala Ser Ser Leu
303                      180                      185                      190
306 His Thr Tyr Thr Cys Asn Val Ser Asn Arg Ala Ser Trp Ala Asn His
307                      195                      200                      205
310 Thr Leu Asn Phe Thr His Gly Cys Gln Ser Val Pro Ser Asn Phe Arg
311                      210                      215                      220
314 Phe Leu Pro Phe Gly Val Ile Ile Val Ile Leu Val Thr Leu Phe Leu
315 225                      230                      235                      240
318 Gly Ala Ile Ile Cys Phe Cys Val Trp Thr Lys Lys Arg Lys Gln Leu
319                      245                      250                      255
322 Gln Phe Ser Pro Lys Glu Pro Leu Thr Ile Tyr Glu Tyr Val Lys Asp
323                      260                      265                      270
326 Ser Arg Ala Ser Arg Asp Gln Gln Gly Cys Ser Arg Ala Ser Gly Ser
327                      275                      280                      285
330 Pro Ser Ala Val Gln Glu Asp Gly Arg Gly Gln Arg Glu Leu Asp Arg
331                      290                      295                      300
334 Arg Val Ser Glu Val Leu Glu Gln Leu Pro Gln Gln Thr Phe Pro Gly
335 305                      310                      315                      320
338 Asp Arg Gly Thr Met Tyr Ser Met Ile Gln Cys Lys Pro Ser Asp Ser
339                      325                      330                      335
342 Thr Ser Gln Glu Lys Cys Thr Val Tyr Ser Val Val Gln Pro Ser Arg
343                      340                      345                      350
346 Lys Ser Gly Ser Lys Lys Arg Asn Gln Asn Tyr Ser Leu Ser Cys Thr
347                      355                      360                      365
350 Val Tyr Glu Glu Val Gly Asn Pro Trp Leu Lys Ala His Asn Pro Ala
351                      370                      375                      380
354 Arg Leu Ser Arg Arg Glu Leu Glu Asn Phe Asp Val Tyr Ser
355 385                      390                      395
358 <210> SEQ ID NO: 5
359 <211> LENGTH: 1147
360 <212> TYPE: DNA
361 <213> ORGANISM: Mus musculus
363 <400> SEQUENCE: 5

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364 atgttggggc aagctgtcct gttcacaacc ttcctgctcc tcagggctca tcagggccaa      60
366 gactgcccag attcttctga agaagtgggt ggtgtctcag gaaagcctgt ccagctgagg      120
368 ccttccaaca tacagacaaa agatgtttct gttcaatgga agaagacaga acaggggtca      180
370 cacagaaaaa ttgagatcct gaattgggtat aatgatgggtc ccagttgggtc aaatgtatct      240
372 tttagtata tctatgggtt tgattatggg gattttgctc ttagtatcaa gtcagctaag      300
374 ctgcaagaca gtggctacta cctgctggag atcaccaaca caggcggaaa agtgtgcaat      360
376 aagaacttcc agcttcttat acttgatcat gttgagaccc ctaacctgaa ggcccagtg      420
378 aagccctgga ctaatgggac ttgtcaactg tttttgtcct gcttggtgac caaggatgac      480
380 aatgtgagct acgccttttg gtacagaggg agcactctga tctccaatca aaggaatagt      540
382 acccactggg agaaccagat tgacgccagc agcctgcaca catacacctg caacgttagc      600
384 aacagagcca gctgggcaaa ccacaccctg aacttcaccc atggctgtca aagtgtccct      660
386 tcgaatttca gatttctgcc ctttgggggtg atcatcgtga ttctagttac attatttctc      720
388 ggggccatca tttgtttctg tgtgtggact aagaagagga agcagttaca gttcagccct      780
390 aaggaacctt tgacaatata tgaatatgtc aaggactcac gagccagcag ggatcaacaa      840
392 gggacaaaga gaattggaca ggcgtgtttc tgaggtgctg gagcagttgc cacagcagac      900
394 tttccctgga gatagaggca ccatgtactc tatgatacag tgcaagcctt ctgattccac      960
396 atcacaagaa aaatgtacag tatattcagt agtccagcct tccaggaagt ctggatccaa     1020
398 gaagaggaac cagaactatt ccttaagttg taccgtgtac gaggaggttg gaaacccatg     1080
400 gctcaaagct cacaaccctg ccaggctgag ccgcagagag ctggagaact ttgatgtcta     1140
402 ctcctag                                     1147

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405 &lt;210&gt; SEQ ID NO: 6

406 &lt;211&gt; LENGTH: 451

407 &lt;212&gt; TYPE: PRT

408 &lt;213&gt; ORGANISM: Artificial Sequence

410 &lt;220&gt; FEATURE:

411 &lt;223&gt; OTHER INFORMATION: Synthetic

414 &lt;220&gt; FEATURE:

415 &lt;221&gt; NAME/KEY: PEPTIDE

416 &lt;222&gt; LOCATION: (1)..(221)

417 &lt;223&gt; OTHER INFORMATION: human NAIL sequences

419 &lt;220&gt; FEATURE:

420 &lt;221&gt; NAME/KEY: PEPTIDE

421 &lt;222&gt; LOCATION: (222)..(451)

422 &lt;223&gt; OTHER INFORMATION: human Fc sequences

424 &lt;400&gt; SEQUENCE: 6

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427 1 5 10 15
430 Tyr Gln Gly Lys Gly Cys Gln Gly Ser Ala Asp His Val Val Ser Ile
431 20 25 30
434 Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val
435 35 40 45
438 Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His
439 50 55 60
442 His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn
443 65 70 75 80
446 Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala
447 85 90 95
450 Ala Gln Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
451 100 105 110

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**VERIFICATION SUMMARY**

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